

#9

1638

D. F. Hall

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,710

DATE: 02/27/2001
TIME: 10:15:25

Input Set : A:\SN09508710seqlist.txt
Output Set: N:\CRF3\02272001\I508710.raw

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MAR 07 2001

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4 <110> APPLICANT: Cole, David
5     Cummins, Ian
6     Edwards, Robert
8 <120> TITLE OF INVENTION: Plant Genes
11 <130> FILE REFERENCE: A33083-PCT-USA 072667.0127
13 <140> CURRENT APPLICATION NUMBER: 09/508,710
14 <141> CURRENT FILING DATE: 2000-07-10
16 <150> PRIOR APPLICATION NUMBER: PCT/GB98/02802
17 <151> PRIOR FILING DATE: 1998-09-16
19 <150> PRTOR APPLICATION NUMBER: GB 971972.1
20 <151> PRIOR FILING DATE: 1997-09-16
22 <160> NUMBER OF SEQ ID NOS: 19
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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27 <211> LENGTH: 1085
28 <212> TYPE: DNA
29 <213> ORGANISM: Triticum aestivum L.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (46)...(711)
34 <223> OTHER INFORMATION: Glutathione S transferase
36 <400> SEQUENCE: 1
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38                                         Met Ala Gly Glu
39                                         1
41 aag ggg ctg ctg ctg gac ttc tgg gtc agc ccg ttc ggg cag cgc      105
42 Lys Gly Leu Val Leu Leu Asp Phe Trp Val Ser Pro Phe Gly Gln Arg
43   5          10          15          20
45 gtc cgc atc gcg ctg gcc gag aag ggc ctg ccc tac qag tac gcg gag      153
46 Val Arg Ile Ala Leu Ala Glu Lys Gly Leu Pro Tyr Glu Tyr Ala Glu
47   25          30          35
49 gag gac ctg atg gcc ggc aag agc gac cgc ctc ctc cgc gcc aac ccg      201
50 Glu Asp Leu Met Ala Gly Lys Ser Asp Arg Leu Leu Arg Ala Asn Pro
51   40          45          50
53 gtc cat aag aag atc ccg gtg ctc ctc cac gac ggc cgt gcc gtc aac      249
54 Val His Lys Ile Pro Val Leu Leu His Asp Gly Arg Ala Val Asn
55   55          60          65
57 gag tcc ctc atc atc ctc cag tac ctg gag gag gcc ttc ccg gac gcg      297
58 Glu Ser Leu Ile Ile Leu Glu Tyr Leu Glu Ala Phe Pro Asp Ala
59   70          75          80
61 ccc gct ctg ctc ccc tcc gac ccc tac gcg cgc gcg cag gcc cgc ttc      345
62 Pro Ala Leu Leu Pro Ser Asp Pro Tyr Ala Arg Ala Gln Ala Arg Phe
63   85          90          95          100
65 tgg gcc gac tac gtc gac aag aag gtc tac gac tgc ggc tcc cgc ctc      393
66 Trp Ala Asp Tyr Val Asp Lys Lys Val Tyr Asp Cys Gly Ser Arg Leu
67   105         110         115
69 tgg aag ctc aag ggc gag cog cag gcg cag gcg cgc gcc gag atg ctg      441

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70	Trp Lys Leu Lys Gly Glu Pro Gln Ala Gln Ala Arg Ala Glu Met Leu			
71	120	125	130	
73	gac atc ctc aag acc ctc gac ggc gcg ctc ggg gac aag ccc ttc ttc		489	
74	Asp Ile Leu Lys Thr Leu Asp Gly Ala Leu Gly Asp Lys Pro Phe Phe			
75	135	140	145	
77	ggc ggc gac aag ttc ggg ttc gtc gac gcc gcc ttc gcg ccc ttc acc		537	
78	Gly Gly Asp Lys Phe Gly Phe Val Asp Ala Ala Phe Ala Pro Phe Thr			
79	150	155	160	
81	qcg tgg ttc cac agc tac gag agg tac ggc gag ttc agc ctg ccg gag		585	
82	Ala Trp Phe His Ser Tyr Glu Arg Tyr Gly Glu Phe Ser Leu Pro Glu			
83	165	170	175	180
85	qtg qcq ccc aag atc gcc gcg tgg gcc aag cgc tyc ggc gag egg gag		633	
86	Val Ala Pro Lys Ile Ala Ala Trp Ala Lys Arg Cys Gly Glu Arg Glu			
87	185	190	195	
89	agc gtc gcc aag agc ctc tac tgg ccg gac aag qtg tac gac ttc atc		681	
90	Ser Val Ala Lys Ser Leu Tyr Ser Pro Asp Lys Val Tyr Asp Phe Ile			
91	200	205	210	
93	ggc ctg ctc aag aag tac ggc atc gag taggcgcgcc gacggacgga		731	
94	Gly Leu Leu Lys Lys Tyr Gly Ile Glu			
95	215	220		
97	cggacggggcc atgcggggcga cagccggggcc gccgtccggga gggaaagcaac aaataaaatca		791	
98	ggggaggcatt tgggtggctt acaaatgcgtta cgctctggata gagtatitct ttcttttttt		851	
99	cttcgtggaa taaaatgtctc cgtgtgtgtg tggttggtgg ttgttgggtt gatcagtca		911	
100	tgtgtgtggg tgcgtgtgt gtatcgtatgt ctcgtgtatgt gtgtgtgtgt caatgtgtca		971	
101	accctggctc tcgggtgggg caacccgaa ttccccacccgtt ccattccatt tccattccgg		1031	
102	gcgtatata aattaaaaaa .gagtctcatt tttttttttt aaaaaaaaaaaa aaaa		1085	
104	<210> SEQ ID NO: 2			
105	<211> LENGTH: 222			
106	<212> TYPE: PRT			
107	<213> ORGANISM: Triticum aestivum L.			
109	<400> SEQUENCE: 2			
110	Met Ala Gly Glu Lys Gly Leu Val Leu Asp Phe Trp Val Ser Pro			
111	1	.5	10	15
112	Phe Gly Gin Arg Val Arg Ile Ala Leu Ala Glu Lys Gly Leu Pro Tyr			
113	20	25	30	
114	Glu Tyr Ala Glu Glu Asp Leu Met Ala Gly Lys Ser Asp Arg Leu Leu			
115	35	40	45	
116	Arg Ala Asn Pro Val His Lys Ile Pro Val Leu Leu His Asp Gly			
117	50	55	60	
118	Arg Ala Val Asn Glu Ser Leu Ile Ile Leu Glu Tyr Leu Glu Glu Ala			
119	65	70	75	80
120	Phe Pro Asp Ala Pro Ala Leu Leu Pro Ser Asp Pro Tyr Ala Arg Ala			
121	85	90	95	
122	Gln Ala Arg Phe Trp Ala Asp Tyr Val Asp Lys Val Tyr Asp Cys			
123	100	105	110	
124	Gly Ser Arg Leu Trp Lys Leu Lys Gly Glu Pro Gln Ala Gln Ala Arg			
125	115	120	125	
126	Ala Glu Met Leu Asp Ile Leu Lys Thr Leu Asp Gly Ala Leu Gly Asp			
127	130	135	140	

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128 Lys Pro Phe Phe Gly Gly Asp Lys Phe Gly Phe Val Asp Ala Ala Phe
129 145 150 155 160
130 Ala Pro Phe Thr Ala Trp Phe His Ser Tyr Glu Arg Tyr Gly Glu Phe
131 165 170 175
132 Ser Leu Pro Glu Val Ala Pro Lys Ile Ala Ala Trp Ala Lys Arg Cys
133 180 185 190
134 Gly Glu Arg Glu Ser Val Ala Lys Ser Leu Tyr Ser Pro Asp Lys Val
135 195 200 205
136 Tyr Asp Phe Ile Gly Leu Leu Lys Lys Tyr Gly Ile Glu
137 210 215 220
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 865
141 <212> TYPE: DNA
142 <213> ORGANISM: Triticum aestivum L.
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (54)...(725)
147 <223> OTHER INFORMATION: WTC 1
149 <400> SEQUENCE: 3
150 ggaactcaac cattgatctt caagaaggcg aagcaaacag agcaaaagggt gtq atq 56
151 55 Met
152 1
154 gcg ccg ccg gtg aag gtg tac qgg tgg qcg atg tcg ccg ttc gtg 104
155 Ala Ala Pro Ala Val Lys Val Tyr Gly Trp Ala Met Ser Pro Phe Val
156 5 10 15
158 gcg ccg ccg ctg ctg tgc ctg gag gag gcc ggc gtg gag tac gag ctc 152
159 Ala Arg Ala Leu Leu Cys Leu Glu Glu Ala Gly Val Glu Tyr Glu Leu
160 20 25 30
162 gtc ccc atg agc ccg gag gcc ggc gac cac ccg cag ccc gac ttc ctc 200
163 Val Pro Met Ser Arg Glu Ala Gly Asp His Arg Gln Pro Asp Phe Leu
164 35 40 45
166 gcc ccg aac ccc ttc ggc cag qtc ccc qtt ctc qag gac ggc gac ctc 248
167 Ala Arg Asn Pro Phe Gly Gln Val Pro Val Leu Glu Asp Gly Asp Leu
168 50 55 60 65
170 acc atc ttc gag tgc ccg gcc qtc gcg agg cac gtg ctg ccg aag cac 296
171 Thr Ile Phe Glu Ser Arg Ala Val Ala Arg His Val Leu Arg Lys His
172 70 75 80
174 aaa ccg gag ctg ctg ggc tcc ggc tcc ccg gag tgc qcg gcg atg gtg 344
175 Lys Pro Glu Leu Leu Gly Ser Gly Ser Pro Glu Ser Ala Ala Met Val
176 85 90 95
178 gac gtq tgg ctg gag gtq gag gcc cac cag cac acc ccg ggc ggc 392
179 Asp Val Trp Leu Glu Val Glu Ala His Gln His Gln Thr Pro Ala Gly
180 100 105 110
182 acc atc gtc atg cag tgc atc ctc acc ccg ttc ctc ggc tgc cag ccg 440
183 Thr Ile Val Met Gln Cys Ile Leu Thr Pro Phe Leu Gly Cys Gln Arg
184 115 120 125
186 gac cag gcc qcc atc gac gag aac gcg qca aag ctg acg aat ctg ttc 488
187 Asp Gln Ala Ala Ile Asp Glu Asn Ala Ala Lys Leu Thr Asn Leu Phe
188 130 135 140 145

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190	gac	gtg	tac	gag	gcg	cgc	ctg	tcg	gag	tac	ctt	gcc	ggg	gag	536		
191	Asp	Val	Tyr	Glu	Ala	Arg	Ieu	Ser	Ala	Ser	Arg	Tyr	Ieu	Ala	Cly	Glu	
192							150				155				160		
194	gcg	gtc	agc	ctc	gcg	gac	ctc	agc	cac	ttc	ccg	ttc	atg	cga	tac	ttc	584
195	Ala	Val	Ser	Ieu	Ala	Asp	Ieu	Ser	His	Phe	Pro	Phe	Met	Arg	Tyr	Phe	
196							165				170				175		
198	atq	gac	acc	gag	tac	gcy	tcg	ctg	gtg	gag	gag	ccg	ccg	cac	gtg	aag	632
199	Met	Asp	Thr	Glu	Tyr	Ala	Ser	Ieu	Val	Glu	Glu	Arg	Pro	His	Val	Lys	
200							180				185				190		
202	gcy	tgg	tgg	gag	gag	ttc	aag	gcc	agc	ccg	ccg	gag	agg	gtg	acg	680	
203	Ala	Trp	Trp	Glu	Glu	Phe	Lys	Ala	Ser	Pro	Ala	Ala	Lys	Arg	Val	Thr	
204							195				200				205		
206	gag	ttc	atq	ccg	cca	aac	ttc	ggg	ttc	gga	aag	aag	gca	gag	aag	725	
207	Glu	Phe	Met	Pro	Pro	Asn	Phe	Gly	Phe	Gly	Lys	Lys	Lys	Ala	Glu	Lys	
208							210				215				220		
210	tgtatqacaag	aac	gca	aaucacc	gac	gca	aat	ttt	gtgtgtgtgt	ctgtgtgtgtgt	ctgtgtgtgtgt	ccgttgttgtgtgt	ccgttgttgtgtgt	ccgttgttgtgtgt	ccgttgttgtgtgt	785	
211	tcaatgtttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	845
212	ttcaaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa	865	
214	<210>	SEQ	ID	NO:	4												
215	<211>	LENGTH:	224														
216	<212>	TYPE:	PRT														
217	<213>	ORGANISM:	Triticum aestivum L.														
219	<400>	SEQUENCE:	4														
220	Met	Ala	Ala	Pro	Ala	Val	Lys	Val	Tyr	Gly	Trp	Ala	Met	Ser	Pro	Phe	
221							1		5		10		15				
222	Val	Ala	Arg	Ala	Leu	Leu	Cys	Leu	Glu	Ala	Gly	Val	Glu	Tyr	Glu		
223							20		25		30						
224	Leu	Val	Pro	Met	Ser	Arg	Glu	Ala	Gly	Asp	His	Arg	Gln	Pro	Asp	Phe	
225							35		40		45						
226	Leu	Ala	Arg	Asn	Pro	Phe	Gly	Gln	Val	Pro	Val	Leu	Glu	Asp	Gly	Asp	
227							50		55		60						
228	Leu	Thr	Ile	Phe	Glu	Ser	Arg	Ala	Val	Ala	Arg	His	Val	Leu	Arg	Lys	
229							65		70		75		80				
230	His	Lys	Pro	Glu	Leu	Leu	Gly	Ser	Gly	Ser	Pro	Glu	Ser	Ala	Ala	Met	
231							85		90		95						
232	Val	Asp	Val	Trp	Leu	Glu	Val	Glu	Ala	His	Gln	His	Gln	Thr	Pro	Ala	
233							100		105		110						
234	Gly	Thr	Ile	Val	Met	Gln	Cys	Ile	Leu	Thr	Pro	Phe	Leu	Gly	Cys	Gln	
235							115		120		125						
236	Arg	Asp	Gln	Ala	Ala	Ile	Asp	Glu	Asn	Ala	Ala	Lys	Leu	Thr	Asn	Leu	
237							130		135		140						
238	Phe	Asp	Val	Tyr	Glu	Ala	Arg	Ieu	Ser	Ala	Ser	Arg	Tyr	Ieu	Ala	Gly	
239							145		150		155		160				
240	Glu	Ala	Val	Ser	Ieu	Ala	Asp	Ieu	Ser	His	Phe	Pro	Phe	Met	Arg	Tyr	
241							165		170		175						
242	Phe	Met	Asp	Thr	Glu	Tyr	Ala	Ser	Ieu	Val	Glu	Glu	Arg	Pro	His	Val	
243							180		185		190						
244	Lys	Ala	Trp	Trp	Glu	Glu	Phe	Lys	Ala	Ser	Pro	Ala	Ala	Lys	Arg	Val	
245							195		200		205						

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246	Thr Glu Phe Met Pro Pro Asn Phe Gly Phe Gly Lys Lys Ala Glu Lys		
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249	<210> SEQ ID NO: 5		
250	<211> LENGTH: 930		
251	<212> TYPE: DNA		
252	<213> ORGANISM: Triticum aestivum L.		
254	<220> FEATURE:		
255	<221> NAME/KEY: CDS		
256	<222> LOCATION: (60)...(725)		
257	<223> OTHER INFORMATION: WIC 2		
259	<400> SEQUENCE: 5		
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261	atg gcg ccg gcg gtg aag gtg tac qgg tgg gcc gtg tgg ccg ttc qtg	107	
262	Met Ala Pro Ala Val Lys Val Tyr Gly Trp Ala Val Ser Pro Phe Val		
263	1 5 10 15		
265	gctt cgc cca ctg ctg tgc ctg gag qag gac ggc qgc gtc gag tac gag ctc	155	
266	Ala Arg Pro Leu Leu Cys Leu Glu Ala Gly Val Glu Tyr Glu Leu		
267	20 25 30		
269	gtg tcc atg agc cgc gcg gcc gac cac cgc cag ccg gac ttc ctc	203	
270	Val Ser Met Ser Arg Ala Ala Gly Asp His Arg Gln Pro Asp Phe Leu		
271	35 40 45		
273	gcc cgg aac ccc ttc ggc cag gtc ccc gtc ctc gag gac ggc gac ctc	251	
274	Ala Arg Asn Pro Phe Gly Gln Val Pro Val Leu Glu Asp Gly Asp Leu		
275	50 55 60		
277	acc ctc ttc gag tcg cgc qcg atc qcg agg cac gtg ctc ccg aag cac	299	
278	Thr Leu Phe Glu Ser Arg Ala Ile Ala Arg His Val Leu Arg Lys His		
279	65 70 75 80		
281	aag ccg qag ctg ctg ggc tgc qgc tcc ccg gag qcg gag qcg atg gtg	347	
282	Lys Pro Glu Leu Gly Cys Gly Ser Pro Glu Ala Glu Ala Met Val		
283	85 90 95		
285	gac gtg tgg ctg gag gtg gag gac cac cag tac aac ccc gctt ggc aac	395	
286	Asp Val Trp Leu Glu Val Glu Ala His Gln Tyr Asn Pro Ala Ala Ser		
287	100 105 110		
289	gcc atc gtg gtg cag tgc atc atc ttg ccg cta ctg ggc ggc gcg cgq	443	
290	Ala Ile Val Val Gln Cys Ile Ile Leu Pro Leu Leu Gly Gly Ala Arg		
291	115 120 125		
293	gac cag gcg gtg gac gag aac gta gcc aag ctc aag aac qtg ctg	491	
294	Asp Gln Ala Val Val Asp Glu Asn Val Ala Lys Leu Lys Lys Val Leu		
295	130 135 140		
297	gag gtg tac gag gca cgg ctg tgc qcg tcc agg tac ctc gtc gcc ggg gac	539	
298	Glu Val Tyr Glu Ala Arg Leu Ser Ala Ser Arg Tyr Leu Ala Gly Asp		
299	145 150 155 160		
301	gac atc agc ctc gcc gac ctc agc cac ttc ccc ttc acg cgc tac ttc	587	
302	Asp Ile Ser Leu Ala Asp Leu Ser His Phe Pro Phe Thr Arg Tyr Phe		
303	165 170 175		
305	atg gag acg gag tac gcg ccg ctg gtg gcg gag ctc ccc cac gtg aac	635	
306	Met Glu Thr Glu Tyr Ala Pro Leu Val Ala Glu Leu Pro His Val Asn		
307	180 185 190		
309	gcy tgg tgg gag ggg ctc aag gcc agg ccg gcc gcy agg aag gtg acg	683	

VERIFICATION SUMMARY
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